GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                      Database :
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      562222 seqs, 172994929 residues
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Gapop 10.0 , Gapext 0.5
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1343
1 YDIGEELGSGQFAIVKKCRE.....
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sp_bacteria:*
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sp_mammal:*
sp_mhc:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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K 9 + > 0 0	001 400	Q98850	Q9C0L5	Q9BE69	P91255	044997	088861	088764	054784	043293	Q9BTL8	Q9CV44	Q9JJP7	Q9QYM4	Q9UIK4	075892	IJ
Galvas identification	Online satting position	Q98850 carassius a	Q9c015 homo sapien	Q9be69 macaca fasc	P91255 caenorhabdi	044997 caenorhabdi	O88861 mus musculu	O88764 rattus norv	O54784 mus musculu	O43293 homo sapien	Q9btl8 homo sapien	Q9cv44 mus musculu	Q9jjp7 mus musculu	Q9qym4 mus musculu		075892 homo sapien	Description

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38.8	39.1	40.0	•	•	•	•	•	41.9	•		42.4	42.7	42.7	42.7	42.7	42.7	42.7	42.7	42.8		•	•	•		•		•	•	
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ALIGNMENTS

Query Match 99.2%; Score 1332; DB 4; Lengt Best Local Similarity 99.6%; Pred. No. 1.5e-95; Matches 262; Conservative 0; Mismatches 1; Inde	RESULT 1 O75892 ID 075892 ID 075892 ID 075892; AC 075892; AC 075892; DT 01-NOV-1998 (TYEMBLIFEL 08, Created) DT 01-NOV-1998 (TYEMBLIFEL 19, Last sequence update) DT 01-DEC-2001 (TYEMBLIFEL 19, Last annotation update) DE DAP-KINASE RELATED PROTEIN 1. OS Homo Sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; EU OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; H OX NCBI_TAXID-9606; RN [1] RN SEQUENCE FROM N.A. RC TISSUE=KINNEY; RX MEDLINE=20094983; PubMed=10629061; RX MEDLINE=20094983; PubMed=1
i; Length 370; i; 1; Indels 0; Gaps	odate) odate) rata; Euteleostomi; inidae; Homo. nidae; Homo. op profein Kinases. kinase; Transferase.

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OGUTK4, PRELIMING.

OGUTK4, PREMITE 1. 13, Created)

OL-MAY-2000 (TrEMBLrel. 13, Last sequence update)

OL-MAY-2001 (TrEMBLrel. 19, Last annotation update)

OL-DEC-2001 (TrEMBLrel. 19, Last annotation update)

OL-MAY-ASSOCIATED PROTEIN KINASE 2.
                                                                                                                                                                                       PRINTS; PRO0109; TYRKINASE.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_DATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; 3

ATP-binding; Kinase; Serine/threonine-protein kinase; 3

ATP-binding; Kinase; Serine/threonine-protein kinase; 3
                                                                                                                                                                                                                                                                   InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                       Oncogene 18:3471-3480(1999).

-- SIMILARITY: BELONGS TO THE

EMBL; AB018001; BAAB8063.1; --

HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-99303018; PubMed-10376525;
Kawai T., Nomura F., Hoshino K., Copeland N.G.,
Jenkins N.A., Akira S.;
                              121
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                                                                                                                                                                                                                                                                                                                                                                  activity.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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KKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNYE
                                                                                                 YDIGEELGSGOFAIVKKCREKSTGLEYAAKFIKKROSRASRRGVSREEIEREVSILROVL
                                          HHNVITLHDVYENRTDVVLILELVSGGELFDFLAQKESLSEEEATSFIKQILDGVNYLHT
                                                       HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKQILDGVNYLHT
                                                                                      YDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVL
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260; Conserv
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Primates;
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                                                                                                                                    Score 1321; DB 4;
Pred. No. 1.1e-94;
1; Mismatches 2;
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Catarrhini;
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R INTERPRO; IPR000719; Euk_pkinase.

R INTERPRO; IPR002290; Ser_thr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Pfam; PF00069; pkinase; 1.

R Pfam; PF00069; TYRKINASE.

R PFINITS; PR00109; TYRKINASE.

R PROSITE; PS00117; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00117; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00118; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00108; TYRE; 1.
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090YM4;
01-MAY-2000 (TIEMBLIEL 13, C
01-MAY-2000 (TIEMBLIEL 13, L
01-DEC-2001 (TIEMBLIEL 19, L
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MEDLINE=99303018; PubMed=10376525;
Momura F., Hoshino K., Copeland
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DEATH-ASSOCIATED PROTEIN KINASE 2.
DAPK2 OR DAPK2.
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Jenkins N.A., Akira S.;
"Death-associated protein kir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10090;
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InterPro; IPR000718; Death.

R InterPro; IPR000719; Ser_thr_pkinase.

R InterPro; IPR0002290; Ser_thr_pkinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R Pfam; PP00023; Ank; 8.

R Pfam; PP00023; Ank; 8.

R Pfam; PP00069; pkinase; 1.

R SMART; SM00248; ANK; 8.

SMART; SM00240; DEATH; 1.

R SMART; SM00208; ANK_REPEAT; 7.

R PROSITE; PS50027; ANK_REP_REGION; 1.

R PROSITE; PS50017; DEATH_DOMAIN; 1.

R PROSITE; PS50017; DEATH_DOMAIN; 1.

R PROSITE; PS50017; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS50018; PROTEIN_KINASE_TO; 1.

R PROSITE; PS00108; PROTEIN_KINASE_TO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 211; Conserv
   Q9CV44;
Q9CV44;
01-JUN-2001
01-JUN-2001
01-DEC-2001
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Q9JJP7;
01-OCT-2000 (TrEMBLrel. 15, Crea:
01-OCT-2000 (TrEMBLrel. 15, Last
01-DEC-2001 (TrEMBLrel. 19, Last
DEATH ASSOCIATED PROTEIN KINASE.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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   (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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Pred. No. 6e-79;
7; Mismatches 15;
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RA Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., RA Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Ra Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Ty T., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Ty T., The Matsuki S., Ty T., Ty T.
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KL Nature 409;685-690(2001).

KL Nature 409;685-690(2001).

KR MGD; MG1:401685; 2310039H24Rik.

KR MGD; MG1:4916885; 2310039H24Rik.

KR MGD; MG1:4916885; 2310039H24Rik.

KR InterPro; IPR000719; Euk_Pkinase.

KR InterPro; IPR000719; Ser_thr_pkinase.

KR InterPro; IPR000290; Ser_thr_pkinase.

KR InterPro; IPR001245; Tyr_pkinase.

KR InterPro; IPR001245; Tyr_pkinase.

KR PRINTS; PR00109; TYRKINASE; I.

KR PRINTS; PR00109; TYRKINASE, I.

KR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.

KR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
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Best Local
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Mammalia; Eutheria;
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2310039H24RIK.
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210; Conserv
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Rodentia;
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Pred. No. 1.6e
38; Mismatches
275
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Sciurognathi; Muridae;
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Submitted (FEB-2001) to the EMBL/GenBan Submitted (FEB-2001) to the SER/THR SUBMILARITY: BELONGS TO THE SER/THR EMBL; BC003614; AAH03614.1; -.
HSSP; Q63450; 1A06.
InterPro; IPR00719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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01-JUN-2001 (TREMBLrel. 19, L
01-DEC-2001 (TREMBLrel. 19, L
SIMILAR TO DEATH-ASSOCIATED PI
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
NCBI_TaxID-0666.
                                                                                                                                             043293
043293;
01-JUN-1998
01-JUN-1998
01-OCT-2001
                                    Homo sapiens (Human).
Homo sapiens (Human).
'--rvota; Metazoa; Chordata;
'--rvota; Primates;
   SEQUENCE
                    NCBI_TaxID=9606;
                                                                                                                               ZIP-KINASE.
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01-JUN-2001
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Primates;
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PROTEIN KINASE 1.
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                                               Craniata; Vertebrata; Catarrhini; Hominidae;
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Best Local Similarity
Matches '210; Conserv
                                                                          Eukaryota; Metazoa; (
Mammalia; Eutheria; F
NCBI_TaxID=10090;
[1]
                                                                                                                                            054784;
054784;
01-JUN-1998
01-JUN-1998
01-DEC-2001
  SEQUENCE FROM N.A.
MEDLINE-98147805; PubMed-9488481;
Kawai T., Matsumoto M., Takeda K., San
"ZIP-kinase, a novel serine/threonine
apoptosis.";
MOI. Cell. Biol. 18:1642-1651(1998).
-I- SIMILARITY: BELONGS TO THE CPD / MUD
                                                                                                                  Mus musculus
                                                                                                                             DAPK3
                                                                                                                                      ZIP-KINASE.
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PROSITE; PS500101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 454 AA; 52535 MW; 56773008A6A6ICFO CRC64;
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InterPro; IPR0002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
SMART; SM00220; S_TKC; 1.
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-- SIMILARITY: BELONGS TO:
EMBL; AB007144; BAA24955.1;
EMBL; AB022341; BAA81746.1;
HSSP; Q63450; 1A06.
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"ZIP Kinase, a novel serine/threonine
apoptosis.",
Mol. Cell. Biol. 18:1642-1651(1998).
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"ZIP kinase identified as a novel
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MEDLINE-99283879; PubMed-10356987;
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18:1642-1651(1998).
BELONGS TO THE SER/THR
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Rodentia;
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79.8%;
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annotation update)
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; Murinae; Mus
  KINASES
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O88764;
O1-NOV-1998 (TrEMBLrel. 08, C
01-NOV-1998 (TrEMBLrel. 08, L
01-DEC-2001 (TrEMBLrel. 19, L
DAP-LIKE KINASE.
Interpro; in control of the property of the pr
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SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SEQUENCE 448 AA; 51421 MW; DA32EF3EB1F20EFC CRC64;
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                                                                                                                                                                                                                      Oncogene 20:2645-2654(1998).

- SIMILARITY: BELONGS TO THE

EMBL: AJ006971; CAA07360.1; -

HSSP: 063450; 1A06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                          InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                 histones.
                                                                                                                                                                                                                                                                                                                                        that is tightly associated
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*Cloning and characterisation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
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Q63450; 1A
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Pred. No. 6.7e-78
4; Mismatches 2
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; Murinae; Rat
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                                                                                                                                 Query Match
Best Local Similarity
Matches 211; Conserv
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R HSSP; P00518; IPHK.

R InterPro; IPR000719; Euk_pkinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R PFAMM; PF00069; pkinase; 1.

R PRIVIS; PR00109; TYRKINASE.

R PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS500108; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DAP-KINASE RELATED PROTEIN 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20094983; PubMed=10629061;
Inbal B., Shani G., Cohen O., Kissil J.L., Kimchi A.;
"Death-associated protein kinase-related protein 1, a
Serine/Threonine kinase involved in apoptosis.";
Mol. Cell. Biol. 20:1044-1054(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
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                                    REEIEREVSILRQVLHHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESLSEEEAT 105
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Pred. No. 6.7e-78;
4; Mismatches 20
                                                                                                                                Score 1073; DB 11;
Pred. No. 1.5e-75;
2; Mismatches 5;
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Sciurognathi; Muridae;
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; Murinae; Mus
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Lerro; IF.

CerPro; IPROUL
InterPro; IPRO02290,
Pfam; PF000531; death; 1.
Pfam; PF000531; death; 1.
Pfam; PF000531; death; 1.
Pfam; PF00069; pkinase; 1.
OR SMART; SM00005; DEATH; 1.
DR SMART; SM00205; S_TRC; 1.
DR SMART; SM00220; S_TRC; 1.
DR SMART; PS50088; ANK_REPEAT; 7.
PROSITE; PS50011; DEATH DOMAIN; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_ST; 1.
ATP-binding; Repeat; Serine/threonine-protein kinase.
ATP-binding; Repeat; Serine/threonine-protein kinase.

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InterPro; IPR000488; Deat
InterPro; IPR000719; Euk
                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2001) to the EMBL/GenBank/DDBJ-1-SIMILARITY: BELONGS TO THE SER/THR FAMILY EMBL: AF043701; AAK18971.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
"Mamsley P., Kramer J.;
"The sequence of C. el
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                investigating biology. The C Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-99069613; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID-6239;
                                  69
                                                       80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a plinvestigating biology. The C. elegans Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
AVYETASDVIIVLELVSGGELFDHVCAKECLDEVEAAAFIKQILLAVRHLHSLHIVHLDI 199
             DYYENRTDVVHILELVSGGELFDFLAQKESLSEEEATSFIKOILDGVNYLHTKKIAHFDL 128
                                                        GQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVL-HHNVITLH
                                           GOFAVVRRVRDRKTGEKYAAKFIKKRRYATSRRGVTRONIEREVRVLOKIRGNSNVVELH
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Q63450; 1A06
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θ) to the
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EMBL/GenBank/DDBJ databases
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Last sequence update)
Last annotation updat
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OF PROTEIN KINASES
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P91255

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Best Local s
Matches 125
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STRAIN-BRISTOL N2;
Fulton B., Wohldmann P
"The sequence of C. el
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
Waterston R.;
"Direct Submission.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ
EMBL; U80022; AAC25886.2; -.
Hypothetical protein.
SEQUENCE 2762 AA; 306525 MW; C964CCEB6D322
          240
                                                            367
                                                                                                            180
                                                                                                                                                              309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The sequence of C. elegans Submitted (JAN-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium,"; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P91255;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
HYPOTHETICAL 306.5 KDA PROTEIN.
                                                                                                                                                                                                                                                              249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                             195
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                     1 YDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318
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                                     | CPVGLSTDMWTVGVISYVLLSGLSPFLGDSDEDTLANVSASDWDFDDPSWDDVSDLAKDF
IRKLLVKETRKRLTIQEALRHPWI
                                                               KNQIVHLDLKPENILLKAKN--SNELKIIDFGLARKLDPKKSVKLLFGTPEFCAPEVVNY
                                                                                                                                                                 TKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNY
                                                                                                                                                                                                                                                                HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKESL-SEEEATSFIKQILDGVNYLH 119
                                                                                                                                                                                                                                      HEKLLNLHEAFDMGNEMWLTEEFVSGGELFEKTLEDDSLMSEEEVRDYMHOTLLGVSHMH
                                                                                                                                                                                                                                                                                                                                     YIIHEELGKGAYGTVYRATEKATGKTWAAKMVQVRP-----GVKKENVIHEISMMNQLH 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                             125;
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DQRATVEECLQHPWI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 47.3
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  61;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 660.5;
Pred. No. 2.8e
51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cosmid F12F3.";
EMBL/GenBank/DDBJ databases.
  263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C964CCEB6D322084
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ); DB 5;
1.8e-42;
les 69;
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                                          426
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992

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Euteleostomi;
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databases. OF PROTEIN

KINASES

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R Pfam; PF00069; pkinase; 1.

R PFAM; PF00069; pkinase; 1.

R PRIMTS; PR00014; FNTYPEIII.

R SMART; SM00409; IG; 1.

R SMART; SM00410; IG_11ke; 1.

R SMART; SM00210; TYFKC; 1.

R SMART; SM00219; TYFKC; 1.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.

R PROSITE; PS00101; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

W ATP-binding; Hypothetical protein; Repeat;

Seilne/threonine-protein kinase; Transferase.

SEQUENCE 641 AA; 72195 MW; 48BAA0621851868E CRC64;
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Best Local
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 72.2 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osada N., Hida M., Kusuda J., Tanuma R., Suzuki Y., Sugano S., Hashimoto K.; "Isolation of full-length cDNA clones fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-FRONTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003600;
InterPro; IPR002290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003961;
InterPro; IPR003599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                  436
                                                                                                                                                                                                                                                                                            318
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                                                                                                                                                                               HPKLVQCVDAFEEKANIVMVLEIVSGGELFERIIDEDFELTERECIKYMRQISEGVEVIH
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                                                                                                                                                                                                                                                                                                                  HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKE-SLSEEEATSFIKQILDGVNYLH 119
IRKLLVKETRKRLTIQEALRHPWI
| || |: || : |:|||:
                                                                            EPIGYATDWWSIGVICYILVSGLSPEMGDNDNETLANVTSATWDFDDEAFDEISDDAKDF
                                                                                                       EPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDF 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127;
                                                                                                                                                                                                                                                                                                                                                                                               YDIEERLGSGKFGQVFRLVEKKTRKIWAGKFFKAYSAK-----EKENIRQEISIMNCLH 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P56276; 1TLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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iPRO03962; FNIII_repeat.
iPRO03961; FN_III.
iPRO03599; Ig.
iPRO03599; Ig_like.
iPR003590; Ser_thr_pkinase.
iPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e EMBL/GenBank/DDBJ
THE SER/THR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 646.5; DB 6
Pred. No. 5.1e-42;
3; Mismatches 80
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OF PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                    435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R InterPro; irnv...

R Pfam; PF00041; fn3; 1.

JR Pfam; PF00047; ig; 2.

Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00014; FNTYPEIII.

DR SMART; SM000409; IG; 3.

DR SMART; SM00409; IG; 3.

DR SMART; SM00220; STKC; 1.

DR SMART; SM00220; TyrKC; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

RW ATP-binding; Immunoglobulin domain; Kinase; Repeat;

KW ATP-binding; Immunoglobulin domain; Kinase; Repeat;

Serine/threonine-protein kinase; Transferase.
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Best Local S
Matches 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000719; Euk_pkinase.
InterPro; IPR003962; FNIII repeat.
InterPro; IPR003961; FN_III.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003598; Ig_c2.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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Q9C0L5;
01-JUN-2001
01-JUN-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kikuchi A., Murata-Hori M., Hosoya H.;
"HeLa myosin light chain kinase.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY
EMBL, AB037663; BAB21504.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P56276; 1TLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         496
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nes 126; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YDIGEELGSGQFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVL
                                                                                                                                                                                                                                                                      TKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTPEFVAPEIVNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISNLLKKDMKNRLDCTQCLQHPWL
                                                                         IRKLLVKETRKRLTIQEALRHPWI
                                                                                                                                                           EPLGLEADMWSIGVITYILLSGASPFLGDTKQETLANITSVSYDFDEEFFSHTSELAKDF
                                                                                                                                                                                                                                     KQGIVHLDLKPENIMCVNKT--GTRIKLIDFGLARRLENAGSLKVLFGTPEFVAPEVINY
                                                                                                                                                                                                                                                                                                                                           HPKLVQCVDAFEEKANIVMVLEIVSGGELFERIIDEDFELTERECIKYMRQISEGVEYIH
                                                                                                                                                                                                                                                                                                                                                                      HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKE-SLSEEEATSFIKQILDGVNYLH 119
                           ISNLLKKDMKNRLDCTQCLQHPWL
                                                                                                                                EPIGYATDMWSIGVICYILVSGLSPFMGDNDNETLANVTSATWDFDDEAFDEISDDAKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                   YDIEERLGSGKFGQVFRLVEKKTRKVWAGKFFKAYSAK-----EKENIRQEISIMNCLH 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 17, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.88;
47.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 642.5;
Pred. No. 1.86
19; Mismatches
                                                                            263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         519
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.8e-41; es 80;

DB 4;

Length Indels

992;

9;

Gaps

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60

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655

239 713

773

CRC64;

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RESULT 15
Q98850
AC Q98850
AC Q98850
DT Q1-FEB
CC ACTINO
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Best Local S
Matches 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00069; pkinase; 1.
SMART; SM00060; FN3; 1.
SMART; SM00408; IGC2; 2.
SMART; SM00220; S_TKc; 1.
PROSITE; PS00107; PROTEIN_K;
PROSITE; PS50011; PROTEIN_K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PSO0107; PROTEIN_KINASE_ATP; UNKNOWN_1.
PROSITE; PSO0101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
ATP-binding; Immunoglobulin domain; Kinase;
Serine/threonine-protein kinase; Transferase.
SEQUENCE 907 AA; 101423 MW; 3B6BA33BF312362C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97067382; PubMed-8910795;
Jian X., Szaro B.G., Schmidt J.T.;
Jian X., Szaro B.G., Schmidt J.T.;
"Myosin 11ght chain kinase: expression in neurons and upregulation during axon regeneration.";
J. Neurobiol. 31:379-391(1996).
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; U61731; AAB41402.1; -.
HSSP; P56276; 1TLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q98850 PRELIMINARY; PRT; 907 AA.
Q98850;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
REURONAL MYOSIN LIGHT CHAIN KINASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-COMMON COMET;
                                                                                                                                                         Pfam; PF00047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF0004
             702
                                                                          240 IRKLLVKETRKRLTIQEALRHPWI 263
                                                                                                                                                                                                                                                                                                                                584 KKGIVHLDLKPENIMCVNKT--GSKIKLIDFGLARRLENAGSLKVLFGTPEFVAPEVINY
                                                                                                                                                                                                                                                                                                                                                                                120 TKKIAHFDLKPENIMLLDKNIPIPHIKLIDFGLAHEIEDGVEFKNIFGTDEFVAPETVNY 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 HHNVITLHDVYENRTDVVHILELVSGGELFDFLAQKE-SLSEEEATSFIKQILDGVNYLH 119 : | : | : | : | : | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 119 | 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YDIGEELGSGGFAIVKKCREKSTGLEYAAKFIKKRQSRASRRGVSREEIEREVSILRQVL 60
ISNLLKKDMKARLSCDQCFQHPWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YDVEDRLGTGKFGAVFKLIEKSTKKVWAGKFIKAYSAK-----EKDNVRQEIAIMNDLR 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000719; Euk_pkinase.
IPR003961; FN_III.
IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR002290;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig_MHC.
Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 636.5; DB 13;
Pred. No. 4.8e-41;
6; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Euteleostomi;
Euteleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                    641
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Search completed: May 18, 2002, 05:11:45 Job time: 1451 sec

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